MycoKeys 83: 123–144 (2021)
doi: 10.3897/mycokeys.83.68582
https://mycokeys.pensoft.net

RESEARCH ARTICLE

A peer-reviewed open-access journal
MycoKeys
Launched to accelerate biodiversity research

Three new species of *Rhytidhysteron* (Dothideomycetes, Ascomycota) from Mexico

Aurora Cobos-Villagrán[1], Ricardo Valenzuela[1], César Hernández-Rodríguez[2], Rosa Paulina Calvillo-Medina[5], Lourdes Villa-Tanaca[2], Luz Elena Mateo-Cid[3], Abigail Pérez-Valdespino[4], César Ramiro Martínez-González[6], Tania Raymundo[1]

1 *Instituto Politécnico Nacional, Escuela Nacional de Ciencias Biológicas, Laboratorio de Micología, Prolongación de Carpio y Plan de Ayala s/n, Mexico City 11340, Mexico* **2** *Instituto Politécnico Nacional, Escuela Nacional de Ciencias Biológicas, Laboratorio Experimental de Bacterias y Levaduras, Prolongación de Carpio y Plan de Ayala s/n, Mexico City 11340, Mexico* **3** *Instituto Politécnico Nacional, Escuela Nacional de Ciencias Biológicas, Laboratorio de Ficología, Prolongación de Carpio y Plan de Ayala s/n, Mexico City 11340, Mexico* **4** *Instituto Politécnico Nacional, Escuela Nacional de Ciencias Biológicas, Laboratorio de Ingeniería Genética, Prolongación de Carpio y Plan de Ayala s/n, Mexico City 11340, Mexico* **5** *Facultad de Química, Universidad Autónoma de Querétaro, Cerro de las Campanas s/n, Querétaro 76010, Mexico* **6** *Universidad Autónoma Chapingo, Departamento de Fitotecnia, Instituto de Horticultura, Km 38.5 Carretera Federal México-Texcoco, Texcoco, Estado de México 56230, Mexico*

Corresponding author: Tania Raymundo (traymundoo@ipn.mx)

Academic editor: Cecile Gueidan | Received 12 May 2021 | Accepted 9 August 2021 | Published 14 September 2021

Citation: Cobos-Villagrán A, Valenzuela R, Hernández-Rodríguez C, Calvillo-Medina RP, Villa-Tanaca L, Mateo-Cid LE, Pérez-Valdespino A, Martínez-González CR, Raymundo T (2021) Three new species of *Rhytidhysteron* (Dothideomycetes, Ascomycota) from Mexico. MycoKeys 83: 123–144. https://doi.org/10.3897/mycokeys.83.68582

Abstract

The genus *Rhytidhysteron* is characterised by forming navicular to apothecial hysterothecia, exposing the green, yellow, orange, red, vinaceous or black colours of the hymenium which generally releases pigments in the presence of KOH. The exciple is smooth or striated, the asci bitunicate and ascospores have 1–5 transverse septa. To date, twenty-six *Rhytidhysteron* species have been described from the Tropics. The present study aims to describe three new species in the Neotropics of Mexico based on molecular methods and morphological features. Illustrations and a taxonomic key are provided for all known species of this genus. *Rhytidhysteron cozumelense* from the Isla Cozumel Biosphere Reserve, *R. esperanzae* from the Sierra Juárez, Oaxaca and *R. mesophilum* from the Sierra Madre Oriental, Hidalgo are described as new species. With the present study, the number of species of *Rhytidhysteron* known from Mexico is now increased to eight.

Keywords

Hysteriaceae, Hysteriales, Neotropic, phylogeny, taxonomy

Copyright *Aurora Cobos-Villagrán et al.* This is an open access article distributed under the terms of the Creative Commons Attribution License (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Introduction

The genus *Rhytidhysteron* was described by Spegazzini (1881) and has been shown to belong to the Hysteriaceae (Boehm et al. 2009a, 2009b; Wijayawardene et al. 2020). The genus is characterised by forming hysterothecia, with lenticular or irregular, striated, or smooth openings; epithecium of various colours; excipulum composed of 1–2 layers of cells of angularis texture or globose texture. *Rhytidhysteron* presents dense hamathecium, composed of branched pseudo-paraphyses, enclosed in a gelatinous matrix; octosporic, bitunicate, cylindrical asci; 1–3 septa ascospores, constricted in the central septum, reddish-brown to brown (Spegazzini 1881; Samuels and Müller 1979; Kutorga and Hawksworth 1997; Boehm et al. 2009b; Thambugala et al. 2016).

The distribution of the genus is Pantropical. It has been reported as an endophytic fungus (Rashmi et al. 2019) and causes mycosis in humans (Chowdhary et al. 2008; Mishra et al. 2014; Mahajan et al. 2014; Chander et al. 2016).

The species with the largest distribution is *Rhytidhysteron rufulum*. It has been described from various places, with slight morphological differences depending on where it was found. *R. rufulum* have hysterothecia 1500–2000 µm long, ascospores of (19–)26–36(–43) µm and the colour of the red epithecium in Melzer's Reagent changes to bright orange (Samuels and Müller 1979). According to Kutorga and Hawksworth (1997), the length of the hysterothecia ranges from 2500–4000 µm, ascospores from (22–)25–35(–39) µm and has dark brown to reddish epithecium in potassium hydroxide (KOH) which changes to pale greenish-brown or from red wine to intense pink. On the other hand, in the description made by Almeida et al. (2014), the size of the ascomata ranges from 800–2500 µm, ascospores from 21–32 µm and has black or red epithecium without extractable KOH pigment. The specimens from Thailand have ascomata from 900–2350 µm, ascospores from 28–36 µm and black or red epithecium are not reported to have a reaction with any reagent (Thambugala et al. 2016). Finally, Cobos-Villagrán et al. (2020), for the Mexican specimens, report ascomata of 1000–3000 µm, ascospores of 22.4–30.4 µm and orange-reddish, yellow or black epithecia changing to magenta in reaction with KOH. These morphological variations within *R. rufulum* have caused confusion in various fungal collections around the world and, as a result, they have been grouped into a complex of species (Boehm et al. 2009b; Murillo et al. 2009; Yacharoen et al. 2015; Doilom et al. 2016; Thambugala et al. 2016; Soto-Medina and Lücking 2017).

Twenty-six species are known worldwide according to the Fungorum Index (2021) and, in the last two years, it has had greater relevance, since at least seven species have been described. In the present work, morphological and molecular analyses of distinct specimens of *Rhytidhysteron* obtained from different locations in Mexico were performed. Phylogenetic relationships were inferred based on internal transcribed spacer (ITS), nuclear large subunit ribosomal DNA (LSU) and elongation factor 1-alpha (tef1). Additionally, a dichotomous key is provided with all the species described so far.

Materials and methods

Study zone

The specimens have been found from three different sites: one from Cozumel Island Biosphere Reserve, Quintana Roo, which is located between coordinates 20°35'20" and 20°17'16" north latitude (N) and –86°43'55" and –87°00'07" west longitude (W). The climate, according to the Köppen system, modified by García (1981), is of the AmW (I) type, warm humid with abundant rain in summer. The average annual temperature is 25.5 °C. Average annual rainfall is 1570 mm (INEGI 2013; García-Martínez et al. 2021). The type of vegetation present in the town of San Gervasio is tropical dry forest, at 0 m above sea level.

The second specimen from La Esperanza, Santiago Comaltepec, Chinantla was collected from the Sierra de Juárez in the State of Oaxaca, between coordinates 17°32' and 17°44' north latitude (N) and –96°16' and –96°36' west longitude (W); altitude between 100 and 3200 m a.s.l. La Esperanza presents different types of climates, the main ones, according to the Köppen system, modified by García (1981), are temperate humid with abundant rain in summer, C (m) and semi-warm humid with rain all year round. The temperature range is 10–26 °C. The range of precipitation is 800–4000 mm (INEGI 2008). The type of vegetation present in the town of La Esperanza is tropical cloud forest, at 1600 m a.s.l.

The last of the specimens is from Laguna de Atezca, Molango de Escamilla, which is located in the Sierra Madre Oriental in the State of Hidalgo, between the coordinates 20°42' and 20°59' of north latitude (N) and –98°41' and –98°53' of West longitude (W), altitude between 300 and 2200 m a.s.l. The Laguna de Atezca presents different types of climates, the main ones, according to the Köppen system, modified by García (1981), are semi-warm humid with rain throughout the year, ACf and temperate humid with abundant rain in summer, C (m). The average annual temperature is 17 °C. Average annual rainfall is 1438 mm (INEGI 2009). The type of vegetation present in the town of Laguna de Atezca is tropical cloud forest, at 1281 m a.s.l.

Morphological study

The specimens were obtained by searching for dry or fallen branches in each of the localities. The material was examined following traditional techniques in mycology (Cifuentes et al. 1986). Photographs were taken using a digital camera (Nikon, D7000, Tokyo, Japan) with an 85 mm macro lens (Nikon, Tokyo, Japan). The fresh collected specimens were used to obtain morphological data such as the colour of the epithecium, growth habit and habitat. Ascomata were measured by a stereomicroscope (Zeiss 475002, Jena, Germany). Cross sections were made in the middle part of the ascomata and mounted on temporary slides in 70% alcohol and 10% KOH. Sections were observed under an optical microscope (Zeiss K-7, Jena, Germany) for the measurement of the characters of taxonomic importance.

DNA extraction, amplification and sequencing

The DNA of each specimen of *Rhytidhysteron* spp. was obtained using the cetyltrimethylammonium bromide (CTAB) method, according to Doyle and Doyle (1987). Three molecular markers were used, the ribosomal large subunit (LSU), the internal transcribed spacer rDNA-ITS1 5.8S rDNA-ITS2 (ITS) and translation elongation translation factor 1-α (*tef1*). The primers used for LSU were LOR0f and LR5r (Vilgalys and Hester 1990), for ITS, these were ITS1f and ITS4r (White et al. 1990; Schoch et al. 2012) and *tef1* EF1-B-F1 and EF1-B-R (Wu et al. 2014). DNA amplifications were performed in a GeneAmp PCR System 9700 thermal cycler (Thermo Fisher Scientific), following recommendations by White et al. (1990) for ITS, Vilgalys and Hester (1990) for LSU and Wu et al. (2014) for *tef1*. The PCR products were verified by agarose gel electrophoresis. The gels were run for 1 h at 95 V cm^{-3} in 1.5% agarose and 1× TAE buffer (Tris Acetate-EDTA). The products were then dyed with GelRed (Biotium, USA) and viewed in a transilluminator (Infinity 300 Vilber, Loumat, Germany). Finally, the products were purified using the ExoSap Kit (Affymetrix, USA) according to the manufacturer's instructions and were prepared for the sequencing reaction using the BigDye Terminator Cycle Sequencing Kit v. 3. 1 (Applied BioSystems). Sequencing was carried out in a genetic analyser (Sanger sequencing) by Macrogen Inc. (Seoul, Korea). The sequences of both strains of each sample were analysed, edited and assembled using BioEdit v. 1.0.5 (Hall 1999) to create consensus sequences. The consensus sequences were compared with those in the GenBank database of the National Center for Biotechnology Information (NCBI) using the BLASTN 2.2.19 tool (Zhang et al. 2000).

Phylogenetic analyses

In order to study phylogenetic relationships, our newly produced sequences of six individuals of *Rhytidhysteron* were added to reference sequences of ITS, LSU and *tef1* (Table 1) deposited in the NCBI database (http://www.ncbi.nlm.nih.gov/genbank/). Each gene region was independently aligned using the online version of MAFFT v7 (Katoh et al. 2002, 2017; Katoh and Standley 2013). Alignments were reviewed in PhyDE (Müller et al. 2005), followed by minor manual adjustments to ensure character homology between taxa. The matrices were formed for ITS by 28 taxa (667 characters), for LSU by 31 taxa (875 characters); while the *tef1* consisted of 24 taxa (896 characters). *Gloniopsis calami* was used as the outgroup. The aligned matrices were concatenated into a single matrix (31 taxa, 2438 characters). Five partitioning schemes were established: one for the ITS, one for the LSU, and three to represent the three codon positions of the *tef1* gene region, which were established using the option to minimize the stop codons with Mesquite v3.2 (Maddison and Maddison 2017). The best evolutionary model for alignment was sought using PartitionFinder (Lanfear et al. 2014, 2017; Frandsen et al. 2015). Phylogeny

Table 1. Species names, strain numbers, isolation source, locality and GenBank accession numbers for the taxa used in this phylogenetic analysis. Sequences generated for this study are in bold.

Species	Isolate No.	LSU	ITS	*tef1*	Source and Locality
Rhytidhysteron bruguierae	MFLUCC 17–1502	MN632453.1	MN632458.1	MN635662.1	Dead stems of *Chromolaena odorata*, Thailand
R. bruguierae	MFLUCC 17–1509	MN632455.1	MN632460.1	-	Dead stems of *Chromolaena odorata*, Thailand
R. bruguierae	MFLUCC 17–1511	MN632454.1	MN632459.1	-	Dead stems of *Chromolaena odorata*, Thailand
R. bruguierae	MFLUCC 17–1515	MN632452.1	MN632457.1	MN635661.1	Dead stems of *Chromolaena odorata*, Thailand
*R. bruguierae**	MFLU 18–0571	NG_068292.1	-	MN077056.1	Submerged branches of *Bruguiera* sp. Thailand
R. camporesii	KUN-HKAS 104277	MN429072.1	MN429069.1	MN442087.1	Dead stems, China
R. chromolanae	MFLUCC 17–1516	MN632456.1	MN632461.1	MN635663.1	Dead stems of *Chromolaena odorata*, Thailand
R. cozumelense	**A. Cobos-Villagrán 951**	**MW9394459**	**MZ056797**	**MZ457338**	**Dead twigs of *Tabebuia rosea*, Mexico**
R. cozumelense	**T. Raymundo 7321**	**MW9394460**	**MZ056798**	**MZ457339**	**Dead twigs of *Tabebuia rosea*, Mexico**
R. erioi	MFLU 16–0584	MN429071.1	MN429068.1	MN442086.1	Dead stems, Thailand
R. esperanzae	**T. Raymundo 6579**	**MW9394457**	**MZ477203**	**MZ457336**	**Dead stems Mexico**
R. esperanzae	**R. Valenzuela 17206**	**MW9394458**	**MZ477204**	**MZ457337**	**Dead stems Mexico**
R. hysterinum	EB 0351	GU397350.1	-	GU397340.1	Dead branches, France
R. hongheense	KUMCC 20–0222	MW264193.1	MW264214.1	MW256815.1	Dead twigs of *Dodonaea*, China
R. hongheense	HKAS112348	MW541820.1	MW541824.1	MW556132.1	Dead twigs of *Dodonaea*, China
*R. magnoliae**	MFLUCC 18–0719	MN989384.1	NR_170019.1	MN997309.1	Dead twigs of *Magnolia grandiflora*, China
*R. mangrovei**	MFLU 18–1894	NG_067868.1	NR_165548.1	MK450030.1	Dead twigs of mangrove, Thailand
R. mesophilum	**A. Trejo 74**	**MW9394461**	**MZ056799**	**MZ457340**	**Dead stems, México**
R. mesophilum	**A. Cobos-Villagrán 1800**	**MW939462**	**MZ056800**	**MZ457341**	**Dead stems, México**
*R. mexicanum**	RV17107.1	MT626026	MT626028	-	Dead wood, Mexico
R. mexicanum	RV17107.2	MT626027	MT626029	-	Dead wood, Mexico
*R. neorufulum**	MFLUCC 13–0216	NG_059649.1	NR_164242.1	KU510400.1	Dead wood, Thailand
R. neorufulum	MFLUCC 13–0221	KU377567.1	KU377562.1	-	Dead wood, Thailand
R. neorufulum	MFLUCC 17–2236	MH063266.1	MH062956.1	-	Dead wood, Thailand
R. opuntiae	GKM 1190	GQ221892.1	-	GU397341.1	Kenya
R. rufulum	MFLUCC 14–0577	KU377565.1	KU377560.1	KU510399.1	Woody litter, Thailand
R. tectonae	MFLUCC 13–0710	KU764698.1	KU144936.1	-	Dead branches, India
*R. thailandicum**	MFLUCC 14–0503	NG_059648.1	NR_164241.1	KU497490.1	Dead wood, Thailand
R. thailandicum	MFLU 19–2373	MN989429.1	MN989428.1	MN989431.1	Dead wood, Thailand
R. thailandicum	MFLUCC 13–0051	MN509434.1	MN509433.1	MN509435.1	Dead wood, Thailand
*Gloniopsis calami**	MFLUCC 15–0739	NG_059715.1	KX669036.1	KX671965.1	Unknown

*Ex-type strains.

was performed with Bayesian inference using MrBayes v3.2.6 x64 (Huelsenbeck and Ronquist 2001). The information block for the matrix includes two independent runs of the MC3 chains using 10 million generations (standard deviation ≤0.1). The convergence of the chains was displayed in Tracer v1 (Rambaut et al. 2014). The highest credibility phylogram of the clades recovered with TreeAnnotator v. 1.8 (Bouckaert et al. 2014) was chosen with a 25% burn-in.

Results

Phylogenetic analysis

The ITS, LSU and *tef1* sequences obtained from *Rhytidhysteron cozumelense*, *Rhytidhysteron esperanzae* and *Rhytidhysteron mesophilum* were deposited in GenBank (Table 1). In the Bayesian analysis, the standard deviation between the chains stabilized at 0.001 after 10 million generations, indicating that MC3 reached a stationary phase. To confirm that the sample size was sufficient, the parameter file was examined in Tracer 1.6 (Rambaut et al. 2014): all parameters had an estimated sample size of over 1,500. The posterior probabilities (PP) obtained were estimated by generating a strict consensus tree in MrBayes. Bayesian inference analysis recovered well-supported clades (PP = 1) of the three species *Rhytidhysteron cozumelense*, *Rhytidhysteron esperanzae* and *Rhytidhysteron mesophilum* (Figure 1).

Taxonomy

Rhytidhysteron cozumelense **Cobos-Villagrán, R. Valenz., Hdz-Rdz., Calvillo-Medina & Raymundo sp. nov**
MycoBank No: 839084
Fig. 2

Diagnosis. Differs from *Rhytidhysteron rufulum* in its host (Bignoniaceae), size of ascomata (2.5–3.5 × 1.1–1.5 × 1.0–1.9 mm), asci (182–191 × 12–13 µm) and its reaction with KOH being faster (one to five seconds).

Type. ***Holotype*****:** Mexico. Quintana Roo, Cozumel Municipality, San Gervasio Chen-tuk archaeological zone, 20°29'50"N, –86°50'39"W, 0 m a.s.l., 21 January 2018, A. Cobos-Villagrán 951 (ENCB), on *Tabebuia rosea* DC. (Bignoniaceae), GenBank: LSU MW9394459, ITS MZ056797, tef1 MZ457338**.**

Description. *Ascomata* hysterothecial to apothecial 2.5–3.5 mm long, 1.1–1.5 mm wide, (0.8)1.0–1.9 mm high, erumpent, solitary, boat-shaped hysterothecia, subglobose, elongated, compressed in the apex, with conspicuous longitudinal groove or cleft and becoming lenticular when mature or exposed to moisture, black, carbonaceous when dry. *Margin* involute, smooth to perpendicularly slightly striated, black. *Exciple* integrated in two layers, the first carbonaceous, glabrous, 45–100 µm thick, wide at the base, composed of pseudoparenchymal cells of *textura prismatica* (iso-radiating cells), thick-walled, the second composed of cells hyaline, thin-walled. *Pseudoparaphyses* up to 2.5 µm wide, filamentous, capitate, hyaline, septate, enclosed in a gelatinous matrix, strongly anastomosed above the asci. *Epithecium* reddish brown (8F7) when fresh, black in old specimens or when dry, becoming greyish magenta (13B5) in the presence of 10% KOH. *Asci* 182–191 × 12–13 µm, bitunicate, cylindrical, hyaline, uniseriate, octosporic, thick-walled, with a sinuous base. *Ascospores* 26–29(–31) × 9–11 (–13) µm, ($\bar{x}$= 28 × 10.2 µm, n = 30), ellipsoidal to fusiform, rounded at both ends, dark brown in colour with three transverse septa, with a thick and smooth wall.

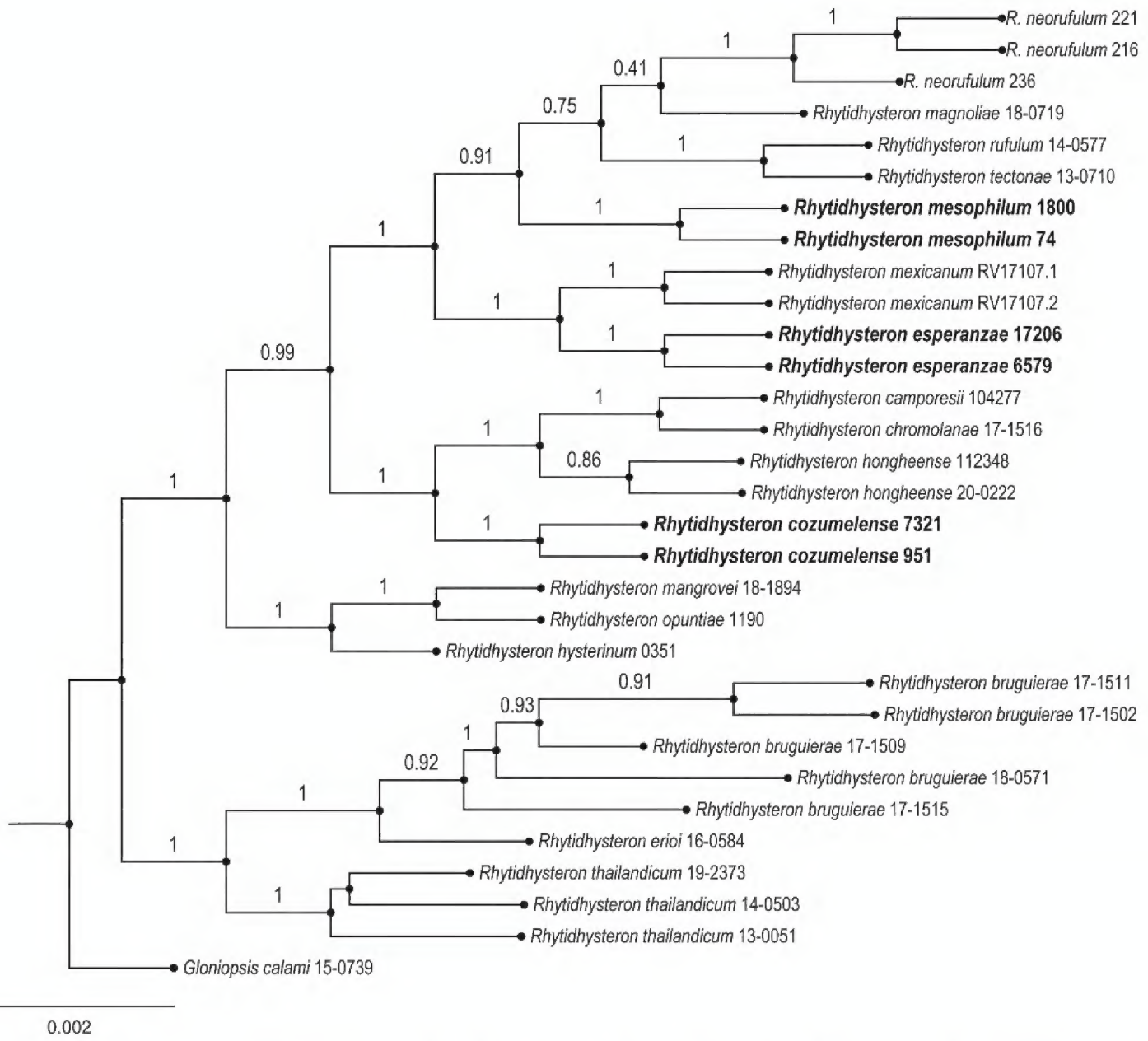

Figure 1. Phylogenetic relationships within the genus *Rhytidhysteron* based on a Bayesian analysis of a combined dataset of ITS, LSU and *tef1* sequence data. *Gloniopsis calami* 150739 was used as the outgroup. The posterior probabilities for each clade are shown above the branches. The new species *Rhytidhysteron cozumelense*, *Rhytidhysteron esperanzae* and *Rhytidhysteron mesophilum* are shown in bold.

Distribution. Known from a single local Island in the Cozumel Biosphere Reserve, Mexico.

Ecology. Dead twigs of *Tabebuia rosea* DC. (Bignoniaceae).

Etymology. The epithet refers to the Island in the Cozumel Biosphere Reserve where the species was found.

Specimens examined. Mexico, Quintana Roo, Cozumel Municipality, San Gervasio Chen-tuk archaeological zone, 20°29'54"N, –86°50'43"W, 13 m a.s.l., 21 January 2018, T. Raymundo 7321, R. Valenzuela 17985 (ENCB); 17 June 2018, A. Cobos-Villagrán 1838 (ENCB).

Notes. *Rhytidhysteron cozumelense* is characterised by black ascomata with a reddish brown epithecium and a smooth to slightly striated margin that, in reaction with 10% KOH, changes to greyish magenta. *R. mesophilum* has a similar reaction in KOH, but with several tones of green in the hysterothecia, a reddish orange to orange red

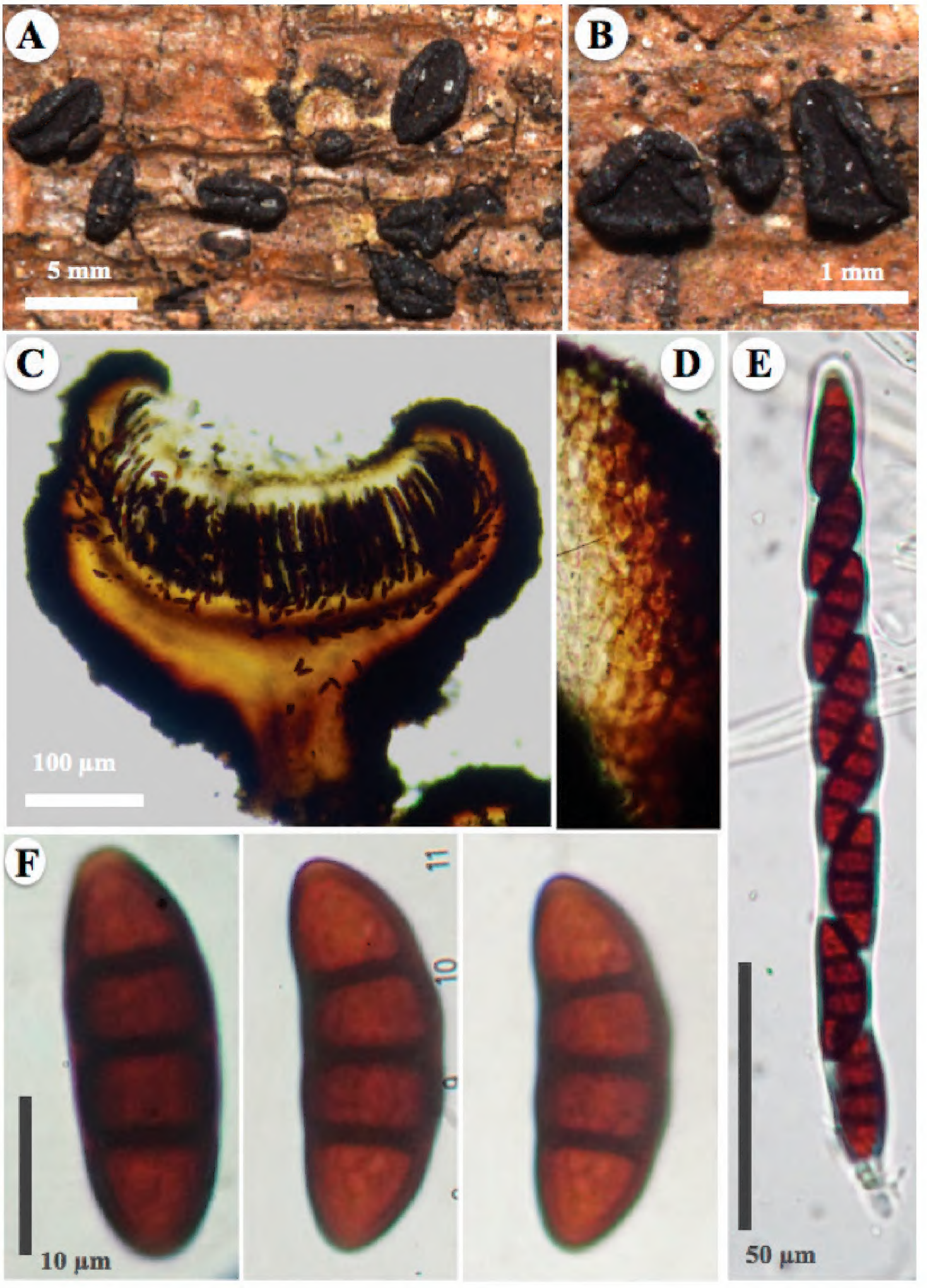

Figure 2. *Rhytidhysteron cozumelense* (Holotype, A. Cobos-Villagrán 951) **A** appearance of ascomata hysterothecial and apothecial on host **B** ascomata apothecial close-up, striated margin and black epithecium **C–F** microscopical features stained with alcohol (70%) and KOH (10%) reagent **C** ascomata apothecial cross-section with alcohol (70%) **D** exciple of iso-radiating cells (*textura prismatica*), close-up **E** asci **F** ascospores.

epithecium and a perpendicularly striate with irregular slits and yellowish green pruina in margin. *R. rufulum* has a magenta reaction in KOH and strongly striated margin. *Tabebuia rosea* is reported as a new host for a *Rhytidhysteron* species.

Rhytidhysteron esperanzae **Cobos-Villagrán, R.Valenz. & Raymundo sp. nov**
Mycobank No: 839086
Fig. 3

Diagnosis. Different from most *Rhytidhysteron* species by having greyish-green ascomata with greenish-grey to yellow epithecium in the presence of KOH, and large and wide ascospores (45–47 × 17–19 µm).

Type. ***Holotype*****:** Mexico. Oaxaca, Sierra de Juárez, Chinantla, Santiago Comaltepec Municipality, La Esperanza, Carretera Oaxaca-Tuxtepec Km 51, 17°37'55"N, –96°22'01"W, 1600 m a.s.l., 23 May 2017, T. Raymundo 6579 (ENCB). GenBank: LSU MW9394457, ITS MZ056795.

Etymology. The epithet refers to the locality "La Esperanza" where the species was found.

Description. *Ascomata* hysterothecial to apothecial, (2–)3–4.5 mm long, (1.2–)2–3 mm wide, (1–)1.7–2.4 mm high, superficial, solitary, rarely gregarious, boat-shaped hysterothecia, elongated, straight or flexuous, with sharp ends, opening in a discoid shape when ripe or with humidity, exposing the hymenium, taking the apothecial shape of 3–4 mm in diameter, brown (6D7), dull-green (30E4) to black. *Margin* involute, perpendicularly striate, greyish green (30C4) to dull green (30D4). *Exciple* integrated in two layers, the first carbonaceous, glabrous, 60–220 µm wide, thinning in the apical part, the middle part and the base are thicker, composed of pseudoparenchymal cells of *textura globulosa-angularis* (isodiametric cells), 11 × 10 µm, thick-walled, 3 µm wide, the second slightly pigmented to hyaline, thin-walled. *Pseudoparaphyses* up to 4 µm wide, filamentous, capitate, apical part wider, straight, hyaline, with a septum, enclosed in a gelatinous matrix, strongly anastomosed above the asci. *Epithecium* dark green (30F4) to black, becoming yellow (2A7) in the presence of 10% KOH. *Asci* (250–)265–270 × (18–)19–20 µm, bitunicate, cylindrical, rounded apex, hyaline, uniseriate, octosporic, thick-walled, with a short pedicel. *Ascospores* of (42–)45–47(–49) × (15–)17–19(–23) µm, ($\bar{x}$ = 45 × 17.2 µm, n = 30), ellipsoidal to spindle-shaped, rounded or pointed at both ends, reddish-brown to brown when mature, with three transverse septa, constricted at the septa, thick-walled and smooth.

Distribution. Known from a single locality in a forest in La Esperanza, Mexico.

Ecology. Dead stems and twigs in tropical cloud forest dominated by *Oreomunnea mexicana* Standl. J.-F. Leroy (Juglandaceae).

Specimens examined. Mexico. Oaxaca. Sierra de Juárez, Santiago Comaltepec Municipality, La Esperanza, Carretera Oaxaca-Tuxtepec Km 51, 17°37'55"N, –96°22'01"W, 1600 m a.s.l., 22 May, 2017, R. Valenzuela 17206 (ENCB); 23 May

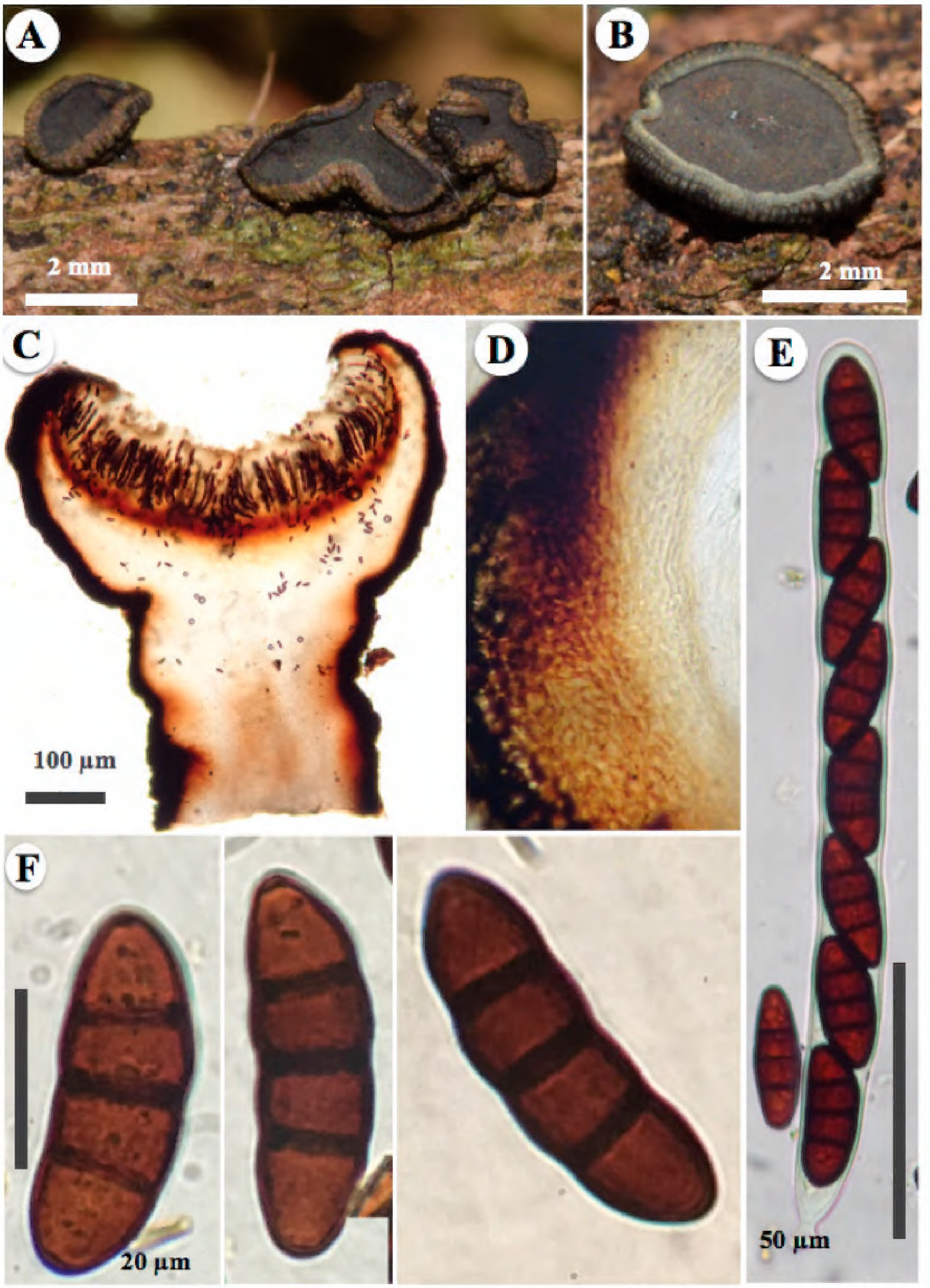

Figure 3. *Rhytidhysteron esperanzae* (Holotype, T. Raymundo 6579) **A** appearance of ascomata apothecial on host **B** ascomata apothecial close-up, greyish-green to dull green and striated margin and dark green to black epithecium **C–F** microscopical features stained with alcohol (70%) and KOH (10%) reagent **C** ascomata apothecial cross-section with alcohol (70%) **D** exciple of isodiametric cells (*textura globulosa-angularis*), close-up **E** asci **F** ascospores.

2017, A. Cobos-Villagrán 498 (ENCB); 25 May 2017, E. Campero 3 (ENCB), 30 April 2018, A. Cobos-Villagrán 1119 (ENCB), A. Gay AG30041814 (ENCB).

Notes. *Rhytidhysteron esperanzae*, is characterised by a brown, dull-green to black exciple and dark green to black epithecium that, in reaction with 10% KOH, changes to yellow colouration. This colouration with KOH is very different than those of of *R. rufulum* and *R. neorufulum* which are magenta and violet, respectively. *R. esperanzae* have larger ascospores than *R. rufulum* (22.4–30.4 × 8–9.6 µm) and *R. mexicanum* (34–40 × 10–12 µm). Ecologically, this new species grows in a tropical cloud forest dominated by *Oreomunnea mexicana* Standl. J.-F. Leroy (Juglandaceae).

Rhytidhysteron mesophilum **Cobos-Villagrán, R. Valenz., Hdz.-Rdz., Calvillo-Medina & Raymundo sp. nov.**

Mycobank No: 839097

Fig. 4

Diagnosis. Differs from *Rhytidhysteron rufulum* by its green-yellowish pruina on the margins, size of asci (267–282 × 15.5–16 µm) and larger ascospores (40–44 × 12–14 µm).

Type. Molango de Escamilla Municipality, Laguna Atezca, 20°48'32"N, –98°44'52"W, 1281 m a.s.l., 01 June 2018, A. Trejo 74 (ENCB). GenBank: LSU MW9394461, ITS MZ056799.

Etymology. The epithet refers to the type of vegetation (mountain mesophilic forest) it was collected from.

Description. *Ascomata* hysterothecial to apothecial, 2.5–4 mm long, 1.0–1.5 mm wide, 1.4–1.7 mm high, superficial or erumpent, gregarious, rarely solitary, with small hysterothecial ascomata, ellipsoid to oblong and black when young, then boat-shaped hysterothecia, with some constriction in the middle part, flexuous, open in apothecioid ascomata, dark green (30F3–4), dull green (30E3–4), greyish green (30E6–7), deep green (30D-E8) to yellowish green (30B-C8) when mature, forming small ascomata within disc in old specimens. *Margin* involute, perpendicularly striate, marks are not roughness, rather irregular slits, with yellowish green (30B-C8) pruina. *Exciple* integrated in two layers, the first carbonaceous, glabrous, green yellowish, 62.5–75 µm thick, in the middle part widening more (112.5–125 µm), composed of pseudoparenchymal cells of *textura prismatica* (isoradiating cells), the second composed of cells hyaline, thin-walled. *Pseudoparaphyses* 2.0–2.5 µm up to 3.0 µm wide, filamentous, capitate, hyaline, without septa, branched towards the apex, enclosed in a gelatinous matrix, strongly anastomosed above the asci. *Epithecium* reddish orange (7B8) to orange red (8A8), becoming greyish magenta (13D6) in the presence of 10% KOH. *Asci* 267–282 × 15.5–16 µm, bitunicate, cylindrical, hyaline, uniseriate, octosporic, thick-walled, with a sinuous base. *Ascospores* (38–)40–44(–46) × 12–14 µm, ($\overline{x}$= 44.2 × 13.6, n = 30), ellipsoidal to oblong, light brown in colour, with three transverse septa, constricted at the septa, with a thick and smooth wall.

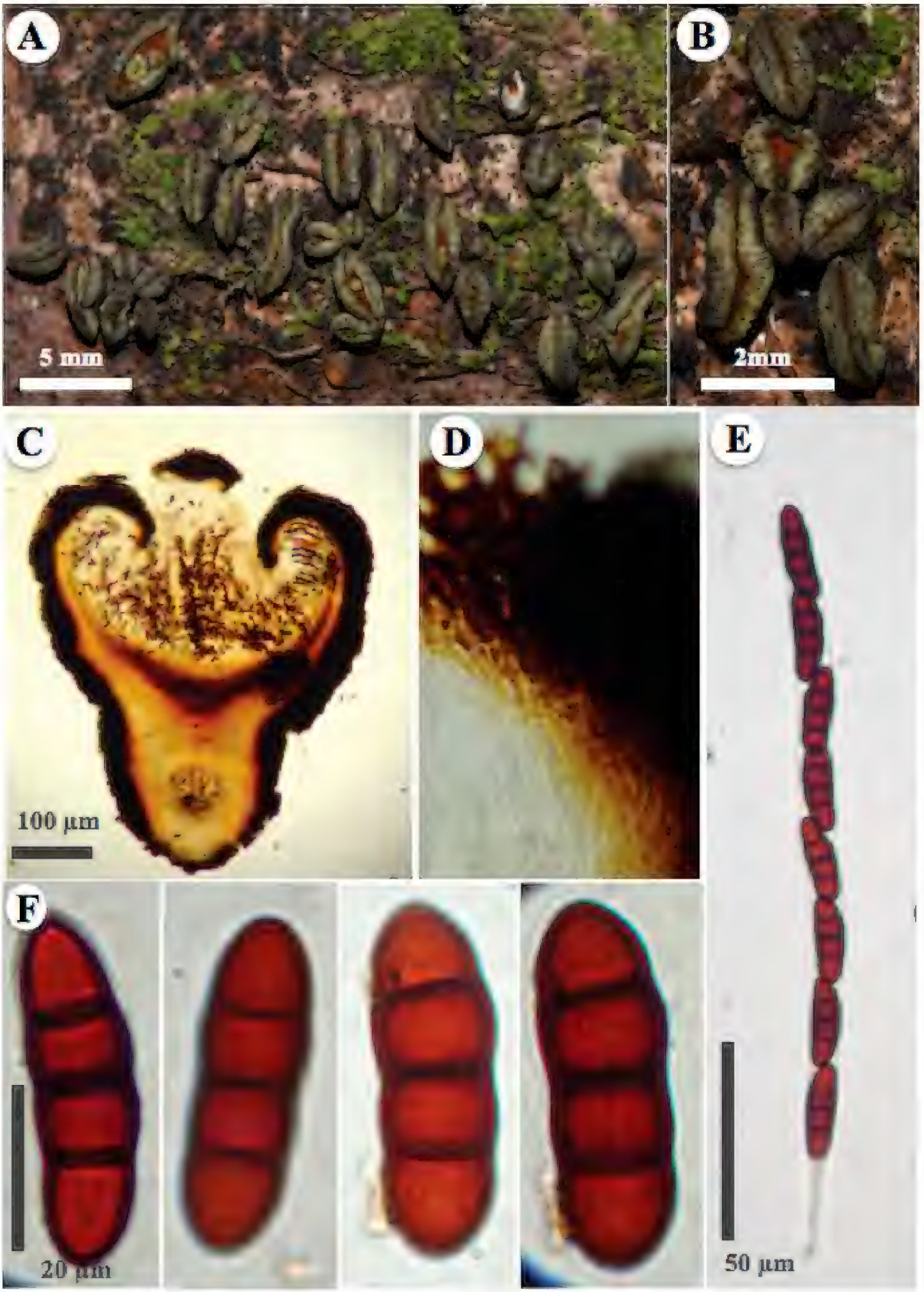

Figure 4. *Rhytidhysteron mesophilum* (Holotype, A. Trejo 74) **A** appearance of ascomata hysterothecial on host **B** ascomata hysterothecial close-up, striated margin with yellowish green pruina and reddish orange to orange red epithecium **C–F** microscopical features stained with alcohol (70%) and KOH (10%) reagent **C** ascomata hysterothecial cross-section with alcohol (70%) **D** exciple of iso-radiating cells (*textura prismatica*), close up **E** asci **F** ascospores.

Distribution. Known from a single locality in Laguna de Atezca, Molango de Escamilla, Hidalgo, Mexico.

Ecology. Dead stems in tropical cloud forest.

Specimens examined. Mexico. Hidalgo, Molango de Escamilla Municipality, Laguna Atezca, 20°48'32"N, –98°44'52"W, 1281 m a.s.l., 01 June 2018; C. Herrera 40 (ENCB), A. Cobos-Villagrán 1800 (ENCB).

Notes. *Rhytidhysteron mesophilum* is characterised by a dark green, dull green, greyish green, deep green to yellowish green hysterothecium, forming small ascomata within disc in old specimens. This fungus could be confused with *R. esperanzae* because both are found in tropical cloud forest (mesophilic forests) and have similar ascospores. However, *R. mesophilum* is distinguished by a reddish orange to orange red epithecium, while in *R. esperanzae*, the epithecium is dark green to black. *R. mesophilum* also resembles *R. columbiense* by the presence of a yellowish green (30B-C8) pruina in the margin, but the ascospores are larger (38–52 × 13–18 µm) and the epithecium is brown to dark brown in the second species.

A dichotomous key is presented with the species of *Rhytidhysteron* accepted by Index Fungorum (2021), including the three new species proposed in this work. The key includes the recently described *R. mexicanum* Cobos-Villagrán, Raymundo, Calvillo-Medina & R. Valenz and *R. hongheense* Wanas. It should be noted that *R. fuscum* (Ellis & Everh.) J.L. Bezerra & Kimbr. and *R. minor* (Cooke) A. Pande are not considered because the first belongs to the genus *Tryblidiella* and the second is a *nom. inval.*, because the basionym was not indicated and bibliographic reference omitted (Art. 41.5, see Art. 41.7, Melbourne).

Key to the known species of *Rhytidhysteron*

1	Ascospores submuriform **2**
–	Ascospores transversely septate, 1–5 septa **3**
2	Ascospores with 3–5 transverse and 1–3 longitudinal septa, 20–25 × 7.5–10 µm, epithecium brown-red, on *Cylindropuntia fulgida*; type: USA ..... ***R. opuntiae* (J.G. Br.) M.E. Barr**
–	Ascospores with 3 transverse septa mainly and rarely with 3 transverse septa and 1 longitudinal septum, 20–33 × 9–13 µm, epithecium reddish orange, on *Dodonaea viscosa*, type: China ..... ***R. hongheense* Wanas.**
3	Ascospores 1–septate **4**
–	Ascospores 3–5 septate **5**
4	Epithecium ferruginous brown, ascospores 22–32 × 10–16 µm, on *Buxus sempervirens*, *Diospyros* spp. or *Ilex* spp.; type: France ..... ***R. hysterinum* (Dufour) Samuels & E. Müll.**
–	Epithecium orange, ascospores 24.8–29(–31) × 8.8–10(–11.2) µm, on *Acacia* spp.; type: Mexico ..... ***R. neohysterinum* Cobos-Villagrán, Hdz.-Rdz., R. Valenz. & Raymundo**
5	Five septa in mature ascospores, 30–46 × 12–20 µm, epithecium yellowish orange, on *Pinus* spp.; type: Finland ..... ***R. dissimile* (P. Karst.) Magnes**
–	Three septa in mature ascospores ..... **f**

6 Ascospores 12–15 × 5–6 µm, exciple brownish green, epithecium brown, on monocotyledonous; type: Sri Lanka ..... ***R. beccarianum*** **(Ces.) Bat. & Valle**

– Ascospores longer than 15 µm **7**

7 Ascospores between 16 to 30 µm long **8**

– Ascospores longer than 30 µm **22**

8 Ascomata with exciple and/or margin in several tones of green **9**

– Ascomata with exciple and margin reddish brown to black **10**

9 Ascomata with exciple and margin vivid green, perpendicularly striate, ascospores 20–30 × 7–9 µm, constricted at the central septum, on angiosperm; type: Brazil..... ***R. viride*** **Speg.**

– Ascomata dark brown to black with yellowish green on the margin, smooth, not striate, ascospores 23–28 × 8–11 µm, slightly constricted at the central septum, on *Chromolaena odorata*; type: Thailand ..... ***R. chromolaenae*** **Mapook & K.D. Hyde**

10 Epithecium with yellow, orange, red or green colour in some development stage..... **11**

– Epithecium brown to black in young and mature specimens..... **18**

11 Epithecium yellowish green, margin perpendicularly striate, ascospores 20.3–30.4 × 7.6–10.1 µm, on *Prosopis jungiflora*; type: USA..... ***R. prosopidis*** **Peck**

– Epithecium with yellow, orange or red colour **12**

12 Ascomata hysterotecial, epithecium yellow, margin smooth, ascospores (19–)28–29(–31) × (8–)10–12(–13) µm constricted at the central septum, on *Tectona grandis*; type: Thailand..... ***R. tectonae*** **Doilom & K.D. Hyde**

– Ascomata apothecial **13**

13 Epithecium with red tones in young or mature specimens **14**

– Epithecium with orange tones in young or mature specimens..... **16**

14 Epithecium vivid red or cinnabar red, ascospores 19.0–24.7 × 7.6–11.4 µm, constricted at the septa, on *Quercus* sp.: type: India..... ..... ***R. quercinum*** **(B.G. Desai & V.N. Pathak) M.P. Sharma & Rawla**

– Epithecium dark red to black..... **15**

15 Growing on mangrove tree, epithecium dark red to dark brown, ascospores 21–28 × 7.5–8.5 µm; type: Thailand ..... ***R. mangrovei*** **Vin. Kumar & K.D. Hyde**

– Growing mainly on Fabaceae, not on mangroves, epithecium orange red, red, dark red to black, 22.4–30.4 × 8–9.6 µm, type: Puerto Rico..... ..... ***R. rufulum*** **(Spreng.) Speg.**

16 Ascospores 28–30 × 10–12 µm, on angiosperm, type: Paraguay..... ..... ***R. discolor*** **(Speg.) Speg.**

– Ascospores smaller than 28 µm **17**

17 Ascospores 6.2–9 µm broad, on *Bruguiera* sp. and *Chromolaena odorata*; type:Thailand..... ***R. bruguierae*** **Dayarathne**

– Ascospores 9–11 µm, on angiosperm; type: Thailand..... ..... ***R. erioi*** **Ekanayaka & K.D. Hyde**

18 Margin perpendicularly striate **19**

– Margin smooth to slightly striate **20**

19 Ascospores 25–27 µm broad, on angiosperm; type: Australia ..... ***R. scortechinii*** **Sacc. & Berl.**

– Ascospores 28–30(–32) µm broad, on *Magnolia grandiflora*; type: China..... ***R. magnoliae*** **N.I. de Silva, Lumyong S & K.D. Hyde**

20 Ascomata apothecial, ascospores 26–29(–31) × 9–11 (–13) µm, on *Tabebuia rosea* DC.; type: Mexico..... ***R. cozumelense*** **Cobos-Villagrán, R.Valenz., Hdz-Rdz., Calvillo-Medina & Raymundo**

– Ascomata hysterotecial **21**

21 Ascospores 25–28 × 9–11 µm, hamathecium release magenta pigment in KOH, on angiosoperm; type: China ..... ***R. camporesii*** **Ekanayaka & K.D. Hyde**

– Ascospores 20–28(-31) × 7.5–12 µm, hamathecium do not release pigment in KOH, on angiosoperm; type: Thailand..... ***R. thailandicum*** **Thambugala & K.D. Hyde**

22 Ascospores 30–40 µm **23**

– Ascospores longer than 40 µm **26**

23 Margin perpendicularly striate, epithecium yellowish green to pistachio green when fresh, light green to pale green when dry, 34–40 × 10–12 µm, on angiosperm; type: Mexico ..... ***R. mexicanum*** **Cobos-Villagrán, Raymundo, Calvillo-Medina & R. Valenz.**

– Margin smooth, epithecium yellow, reddish orange or black..... **24**

24 Epithecium yellow, orange to reddish orange, ascospores 27–34 × (6.5–)7–10.6 (–12.5) µm, on angiosperm; type: Thailand ..... ***R. neorufulum*** **Thambugala & K.D. Hyde**

– Epithecium black **25**

25 Ascospores 10–12 µm broad, constricted at the central septum, on angiosperm; type: Paraguay ..... ***R. guaraniticum*** **Speg.**

– Ascospores 13–14 µm broad, constricted at the septa, on *Scutia indica*; type: India..... ***R. indicum*** **(Anahosur) M.P. Sharma & K.S. Thind**

26 Exciple black, epithecium black, ascospores 40–45 × 15–20 µm, on angiosperm; type: Brazil ..... ***R. brasiliense*** **Speg.**

– Exciple or margin with green tones **27**

27 Exciple and margin dark green, dull green, greyish green, deep green to yellowish green when mature, epithecium reddish orange to orange red, ascospores (38–)40–44(–46) × 12–14 µm, on angiosperm; type: Mexico..... ***R. mesophilum*** **Cobos-Villagrán, R. Valenz., Hdz.-Rdz., Calvillo-Medina & Raymundo**

– Exciple brown, dark brown to black **28**

28 Margin with a yellowish-green pruina, epithecium brown to dark brown, ascospores 38–52 × 13–18 µm, on angisoperm; type: Colombia..... ***R. columbiense*** **Soto-Medina & Lücking**

– Margin greyish green to dull green, epithecium dark green (30F4) to black, ascospores (42–)45–47(–49) × (15–)17–19(–23) µm, on angiosperm; type: Mexico..... ***R. esperanzae*** **Cobos-Villagrán, R.Valenz. & Raymundo**

Discussion

The genus *Rhytidhysteron* is a highly diverse group with a mainly Pantropical distribution (Samuels and Müller 1979). The morphological characteristics that have, so far, helped in the segregation of the species are: shape and border of the hysterothecium, ornamentation of the exciple, colour and reaction of the epithecium, and size of the ascospores which only, in some cases, have helped delimiting species, as in the case of *Rhytidhysteron columbiense* Soto-Medina & Lücking and *R. neohysterinum* Cobos-Villagrán, Hern-Rodr., R. Valenz. & Raymundo.

Therefore, species in which the size of spores overlap, have been clarified by molecular methods and the use of molecular markers, such as ITS, LSU, elongation factor 1 alpha (TEF1), amongst others. For example, in the case of *R. rufulum*, catalogued as a species complex based on morphology, the fungal barcodes have been helpful in describing different species that are morphologically similar (Boehm et al. 2009b; Murillo et al. 2009; Yacharoen et al. 2015; Doilom et al. 2016; Thambugala et al. 2016; Soto-Medina and Lücking 2017). In recent years, part of the taxonomy has been resolved using collections from different countries around the globe. For example, in Thailand, *R. neorufulum* and *R. thailandicum* were described in the work of Thambugala et al. 2016. In the same year, Doilom et al. (2016) described *R. tectone* on *Tectona grandis* L. (Verbenaceae) also from Thailand.

In recent years, eight new species were described: Kumar et al. (2019) described *R. mangrovei* Vinit & K.D. Hyde, isolated from dead mangrove branches; Dayarathne et al. (2020) described *R. bruguierae* Dayarathne, also isolated from mangrove branches *Bruguiera* Lam. (Rhizophoraceae); Hyde et al. (2020) described *R. camporesii* Ekanayaka & K.D. Hyde and *R. erioi* Ekanayaka & K.D. Hyde; Mapook et al. (2020) described *R. chromolaenae* Mapook & K.D. Hyde, isolated from branches of *Chromolaena odorata* (L.) King & Robinson (Asteraceae); Wanasinghe et al. (2021) described *R. hongheense* Wanas. isolated from dead twigs of *Dodonaea* Mill. (Sapindaceae); and in Mexico, Cobos-Villagrán et al. (2020) described *R. neohysterinum* Cobos-Villagrán, Hdez.-Rdz., R. Valenz. & Raymundo and Cobos-Villagrán et al. (2021) *R. mexicanum* Cobos-Villagrán, Raymundo, Calvillo-Medina & R. Valenz. With this new study, three more species have been described from Mexico.

In the present study, we observed that *R. cozumelense* is phylogenetically close to *R. hongheense*, *R. camporesii* and *R. chromolaenae*. The four species are similar in terms of ascospore size in the range of 23–30 × 8–13 µm and have a margin smooth to slightly striate. *R. hongheense* has slightly longer ascospores (20–33 × 9–13 µm). However, they have ascomata of contrasting sizes. *R. chromolaenae* forms smaller navicular hysterothecia, 750–885 µm diam., with orange epithecium, turning purple in KOH and is described from Chiang Rai Province, Thailand (Mapook et al. 2020). *R. camporesii* has hysterothecial ascomata of 800–1100 µm long with black epithecium that changes to magenta in KOH and it is described from Yunnan Province, China (Hyde et al. 2020). Finally, *R. hongheense* has ascomata hystherothecial 1200–2000 µm long with reddish-orange epithecium and it is described from Honghe County, Yunnan Province, China (Wanasinghe et al. 2021). *R. cozumelense* produces longer ascomata, hysterothecial to

apothecial, 2500 to 3500 µm long with reddish brown to black epithecium that changes to greyish magenta in KOH and it grows on *Tabebuia rosea* DC. (Bignoniaceae).

R. esperanzae is phylogenetically close to *R. mexicanum*, both species described from Mexico presenting similar hysterothecial to apothecial ascomata, sizes of 2000–4500 × 1200–2500 µm and a perpendicularly striate margin. However, they differ by the colour of the ascomata and the epithecium: in *R. esperanzae*, the ascomata is brown, the exciple dull-green to black, and the epithecium dark green to black, with a yellow reaction in KOH. In contrast, in *R. mexicanum*, the exciple is completely black and the epithecium yellowish green to pistachio green when fresh, light green, pale green to lemon yellow when dry, becoming ocher to yellow gold in KOH. Another difference is the size of the ascospores which are longer and wider in *R. esperanzae*: they are (42–)45–47(–49) × (15–)17–19(–23) µm, while in *R. mexicanum*, they are 34–40(–44) × 10–12(–15) µm (Cobos-Villagrán et al. 2021).

On the other hand, *R. mesophilum* is characterised by navicular hysterothecia, striated margin with green-yellowish pruina, reddish orange to orange red epithecium that changes to greyish magenta in KOH, and long ascospores. It is related phylogenetically to *R. tectonae* and *R. rufulum*. However, it is morphologically different, including in the size and colour of the hysterothecium, colour of the epithecium, colouration in the reaction with 10% KOH and the size of asci and ascospores. The hysterothecia of *R. tectonae* are 1225–3365 µm long, with a smooth margin, yellow epithecium without reaction in KOH, ascospores (19–)28–29(–31) × (8–)10–12(–13) µm and the species grows on *Tectona grandis* L., in Chiang Rai, Thailand (Doilom et al. 2016). In *R. rufulum*, the size of the ascomata ranges from 1500–2000 µm long, the exciple is black, the epithecium brown, orange, or reddish, changing to magenta in KOH, and the ascospores are 21–32(–39) × 8–9.6 µm (Kutorga and Hawksworth 1997; Almeida et al. 2014; Thambugala et al. 2016; Cobos-Villagrán et al. 2020). In contrast, the hysterothecia of *R. mesophilum* are 2500–4000 µm long, the epithecium orange, changing to greyish magenta in KOH, and the ascospores (38–)40–44(–46) × 12–14 µm, therefore much longer and wider.

In Mexico, the tropical dry forest is the best represented vegetation with four *Rhytidhysteron* species: *R. cozumelense*, *R. neorufulum*, *R. rufulum* and *R. neohysterinum*. This is followed by the xerophilous scrub with *R. thailandicum*, *R. rufulum* and *R. neohysterinum*, and only *R. mexicanum* in *Quercus* forest. Finally, in this study, we describe *R. esperanzae* and *R. mesophilum* in a tropical cloud forest, which is a vulnerable ecosystem and therefore these species are in danger of extinction. With the present study, the number of *Rhytidhysteron* species known from Mexico reaches a total of eight and together with Thailand, they form the countries with the most species diversity of the genus.

Acknowledgements

Dr. T. Raymundo and Dr. R. Valenzuela gratefully acknowledge the financial support received from CONACYT and IPN of Project 252934, and Projects SIP-20210315 and SIP-20210661, respectively. Dr. C. Hernández Rodríguez, Dr. L. Villa Tanaca,

Dr. L. E. Mateo Cid and Dr. A. Pérez Valdespino thank IPN for financial support for their research of the Projects SIP 20200782, SIP-20210508, SIP-20210885 and SIP-20210609, respectively. Dr. Calvillo Medina thanks CONACYT Postdoctoral scholarship (005352). Cobos Villagrán thanks Posgrado en Biociencias, Escuela Nacional de Ciencias Biológicas, IPN. The authors gratefully acknowledge the Sistema Nacional de Investigadores (CONACYT) and COFAA (IPN).

References

Almeida DAC, Gusmão LFP, Miller AN (2014) Brazilian Semi-Arid Ascomycetes I: new and interesting records of hysteriaceous ascomycetes. Mycosphere 5(2): 379–391. https://doi.org/10.5943/mycosphere/5/2/11

Boehm EWA, Mugambi GK, Miller AN, Huhndorf SM, Marincowitz S, Spatafora JW, Schoch CL (2009a) A molecular phylogenetic reappraisal of the Hysteriaceae, Mytilinidiaceae and Gloniaceae (Pleosporomycetidae, Dothideomycetes) with keys to world species. Studies in Mycology 64: 49–83. https://doi.org/10.3114/sim.2009.64.03

Boehm EWA, Schoch CL, Spatafora JW (2009b) On the evolution of the Hysteriaceae and Mytilinidiaceae (Pleosporomycetidae, Dothideomycetes, Ascomycota) using four nuclear genes. Mycological Research 113: 461–479. https://doi.org/10.1016/j.mycres.2008.12.001

Bouckaert R, Heled J, Kühnert D, Vaughan T, Wu C-H, Xie D, Suchard MA, Rambaut A, Drummond AJ (2014) BEAST 2: A software platform for Bayesian Evolutionary analysis. PLOS Computational Biology 10: e1003537. https://doi.org/10.1371/journal.pcbi.1003537

Calvillo-Medina RP, Cobos-Villagrán A, Raymundo T (2020) *Periconia citlaltepetlensis* sp. nov. (Periconiaceae, Pleosporales): a psychrotolerant fungus from high elevation volcanic glacier (Mexico). Phytotaxa 459(3): 235–247. https://doi.org/10.11646/phytotaxa.459.3.5

Chander J, Singla N, Kundu R, Handa U, Spoorthy RCY (2017) Phaeohyphomycosis caused by *Rhytidhysteron rufulum* and review of literature. Mycopathologia 182: 403–407. https://doi.org/10.1007/s11046-016-0064-x

Chowdhary A, Guarro J, Randhawa HS, Gené J, Cano J, Jain RK, Kumar S, Khanna G (2008) A rare case of chromoblastomycosis in a renal transplant recipient caused by a non-sporulating species of *Rhytidhysteron*. Medical Mycology 46: 163–166. https://doi.org/10.1080/13693780701630420

Cifuentes J, Villegas M, Pérez-Ramírez L (1986) Hongos. In: Lot A, Chiang F (Eds) Manual de Herbario. Consejo Nacional de la Flora de México AC, Ciudad de México, 55–64.

Cobos-Villagrán A, Hernández-Rodríguez C, Valenzuela R, Villa-Tanaca L, Calvillo-Medina RP, Mateo-Cid LE, Martínez-Pineda M, Raymundo T (2020) El género *Rhytidhysteron* (Dothideomycetes, Ascomycota) en México. Acta Botanica Mexicana 127: e1675. https://doi.org/10.21829/abm127.2020.1675

Cobos-Villagrán A, Raymundo T, Calvillo-Medina RP, Valenzuela R (2021) *Rhytidhysteron mexicanum* sp. nov. (Dothideomycetes, Ascomycota) from the Sierra of Guadalupe, Trans Mexican Volcanic Belt. Phytotaxa 479(3): 275–286. https://doi.org/10.11646/phytotaxa.479.3.4

Dayarathne MC, Jones EG, Maharachchikumbura SSN, Devadatha B, Sarma VV, Khongphinitbunjong K, Chomnunti P, Hyde KD (2020) Morpho-molecular characterization of

microfungi associated with marine based habitats. Mycosphere 11(1): 1–188. https://doi.org/10.5943/mycosphere/11/1/1

De Silva NI, Tennakoon DS, Thambugala KM, Karunarathna SC, Lumyong S, Hyde KD (2020) Morphology and multigene phylogeny reveal a new species and a new record of *Rhytidhysteron* (Dothideomycetes, Ascomycota) from China. Asian Journal of Mycology 3(1): 295–306. https://doi.org/10.5943/ajom/3/1/4

Doilom M, Dissanayake AJ, Wanasinghe DN, Boonmee S, Liu JK, Bhat DJ, Taylor JE, Bahkali AH, McKenzie EHC, Hyde KD (2016) Microfungi on *Tectona grandis* (teak) in northern Thailand. Fungal Diversity 82: 107–182. https://doi.org/10.1007/s13225-016-0368-7

Frandsen PB, Calcott B, Mayer C, Lanfear R (2015) Automatic selection of partitioning schemes for phylogenetic analyses using iterative k-means clustering of site rates. BMC Evolutionary Biology 15(1): 1–17. https://doi.org/10.1186/s12862-015-0283-7

García E (1981) Modificaciones al sistema de clasificación climática de Köppen (para la República Mexicana). Instituto de Geogeográfia, Universidad Nacional Autónoma de México. Ciudad de México-México, 252 pp.

García-Martínez YA, Heredia Abarca G, Guzmán-Guillermo J, Valenzuela R, Raymundo T (2021) Hongos asociados al mangle rojo *Rhizophora mangle* (Rhizophoraceae) en la Reserva de la Biosfera Isla Cozumel, Quintana Roo, México. Acta Botanica Mexicana 128: e1792. https://doi.org/10.21289/abm128.2021.1792

GenBank (2020) from the NCBI databases. http://www.ncbi.nlm.nih.gov/genbank/ [Accessed on 24.06.2021]

Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98. http://brownlab.mbio.ncsu.edu/JWB/papers/1999hall1.pdf

Hyde KD, Jones EBG, Liu JK, Ariyawansa HA, Boehm E, Boonmee S, Braun U, Chomnunti P, Crous PW, Dai DQ, Diederich P, Dissanayake AJ, Doilom M, Doveri F, Hongsanan S, Jayawardena R, Lawrey JD, Li YM, Liu YX, Lücking R, Monkai J, Muggia L, Nelsen MP, Pang KL, Phookamsak R, Senanayake I, Shearer CA, Seutrong S, Tanaka K, Thambugala KM, Wijayawardene NN, Wikee S, Wu HX, Zhang Y, Aguirre-Hudson B, Alias SA, Aptroot A, Bahkali AH, Bezerra JL, Bhat JD, Camporesi E, Chukeatirote E, Gueidan C, Hawksworth DL, Hirayama K, De Hoog S, Kang JC, Knudsen K, Li WJ, Li X, Liu ZY, Mapook A, McKenzie EHC, Miller AN, Mortimer PE, Phillips AJL, Raja HA, Scheuer C, Schumm F, Chomnunti JE, Tian Q, Tibpromma S, Wanasinghe DN, Wang Y, Xu JC, Yan J, Yacharoen S, Zhang M (2013) Families of Dothideomycetes. Fungal Diversity 63: 1–313. https://doi.org/10.1007/s13225-013-0263-4

Huelsenbeck JP, Ronquist F (2001) Mr Bayes: Bayesian inference of phylogeny. Bioinformatics 17(8): 754–755. https://doi.org/10.1093/bioinformatics/17.8.754

Hyde KD, Dong Y, Phookamsak R, Jeewon R, Bhat DJ, Jones EBG, Liu N-G, Abeywickrama PD, Mapook A, Wei D, Perera RH, Manawasinghe IS, Pem D, Bundhun D, Karunarathna A, Ekanayaka AH, Bao D-F, Li J, Samarakoon MC, Chaiwan N, Lin C-G, Phutthacharoen K, Zhang S-N, Senanayake IC, Goonasekara ID, Thambugala KM, Phukhamsakda C, Tennakoon DS, Jiang H-B, Yang J, Zeng M, Huanraluek N, Liu J-K, Wijesinghe SN, Tian Q, Tibpromma S, Brahmanage RS, Boonmee S, Huang S-K, Thiyagaraja V, Lu Y-Z, Jayawardena RS, Anand G, Devadatha B, Niranjan M, Sarma VV, Liimatainen K, Aguirre-Hudson,

B, Niskanen T, Overall A, Mendes-Alvarenga RL, Baptista-Gibertoni T, Pfliegler WP, Horváth E, Imre A, Alves AM, da Silva-Santos AC, Vieira-Tiago P, Bulgakov TS, Wanasinghe DN, Bahkali AH, Doilom M, Elgorban AM, Maharachchikumbura SSN, Rajeshkumar C, Haelewaters D, Mortimer PE, Zhao Q, Lumyong S, Xu J, Sheng J (2020) Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 100: 5–277. https://doi.org/10.1007/s13225-020-00439-5

Index Fungorum (2021) Index Fungorum. http://www.indexfungorum.org/names/Names.asp [Accessed on 24.06.2021]

INEGI (2008) Prontuario de información geográfica municipal de los Estados Unidos Mexicanos. Santiago Comaltepec, Oaxaca. http://www3.inegi.org.mx/contenidos/app/mexicocifras/datos_geograficos/20/20458.pdf [Accessed on 11.03.2021]

INEGI (2009) Prontuario de información geográfica municipal de los Estados Unidos Mexicanos. Molango de Escamilla, Hidalgo. http://www3.inegi.org.mx/contenidos/app/mexicocifras/datos_geograficos/13/13042.pdf [Accessed on 11.03.2021]

INEGI (2013) Conociendo Quintana Roo, México. Instituto Nacional de Estadística y Geografía. http://internet.contenidos.inegi.org.mx/contenidos/productos/prod_serv/contenidos/espanol/bvinegi/productos/estudios/conociendo/QUINTANA_ROO.pdf [Accessed on 11.03.2021]

Katoh K, Misawa K, Kuma K, Miyata T (2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Research 30(14): 3059–3066. https://doi.org/10.1093/nar/gkf436

Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Molecular Biology and Evolution 30(4): 772–780. https://doi.org/10.1093/molbev/mst010

Katoh K, Rozewicki J, Yamada, KD (2017) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics: bbx108. https://doi.org/10.1093/bib/bbx108

Kumar V, Cheewangkoon R, Thambugala KM, Jones GEB, Brahmanage RS, Doilom M, Jeewon R, Hyde KD (2019) *Rhytidhysteron mangrovei* (Hysteriaceae), a new species from mangroves in Phetchaburi Province, Thailand. Phytotaxa 401: 166–178. https://doi.org/10.11646/phytotaxa.401.3.2

Kutorga E, Hawksworth DL (1997) A reassessment of the genera referred to the family Patellariaceae (Ascomycota). Systema Ascomycetum 15: 1–110.

Lanfear R, Calcott B, Kainer D, Mayer C, Stamatakis A (2014) Selecting optimal partitioning schemes for phylogenomic datasets. BMC Evolutionary Biology 14(1): 82. https://doi.org/10.1186/1471-2148-14-82

Lanfear R, Frandsen PB, Wright AM, Senfeld T, Calcott B (2017) Partition Finder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. Molecular Biology and Evolution 34(3): 772–773. https://doi.org/10.1093/molbev/msw260.

Maddison WP, Maddison DR (2017) Mesquite: a modular system for evolutionary analysis. Version 3.31. http://mesquiteproject.org

Mahajan VK, Sharma V, Prabha N, Thakur K, Sharma NL, Rudramurthy SM, Chauhan PS, Mehta KS, Abhinav C (2014) A rare case of subcutaneous phaeohyphomycosis caused by a

Rhytidhysteron species: a clinico-therapeutic experience. International Journal of Dermatology 53: 1485–1489. https://doi.org/10.1111/ijd.12529

Mapook A, Hyde KD, McKenzie EHC, Jones EBG, Bhat DJ, Jeewon R, Stadler M, Samarakoon MC, Malaithong M, Tanunchai B, Buscot F, Wubet T, Purahong W (2020) Taxonomic and phylogenetic contributions to fungi associated with the invasive weed *Chromolaena odorata* (Siam weed). Fungal Diversity 101: 1–175. https://doi.org/10.1007/s13225-020-00444-8

Mishra K, Das S, Goyal S, Gupta C, Rai G, Ansari MA, Singal A (2014) Subcutaneous mycoses caused by *Rhytidhysteron* species in an immunocompetent patient. Medical Mycology Case Reports 5: 32–34. https://doi.org/10.1016/j.mmcr.2014.07.002

Müller K, Quandt D, Müller J, Neinhuis C (2005) PhyDE-Phylogenetic data editor. Program distributed by the authors, version 10.0. https://www.phyde.de

Murillo C, Federico JA, Julieta C, Thorsten L, Giselle T (2009) Molecular data indicate that *Rhytidhysteron rufulum* (ascomycetes, Patellariales) in Costa Rica consists of four distinct lineages corroborated by morphological and chemical characters. Mycological Research 113: 405–416. https://doi.org/10.1016/j.mycres.2008.09.003

Posada D (2008) jModelTest: phylogenetic model averaging. Molecular Biology and Evolution 25: 1253–1256. https://doi.org/10.1093/molbev/msn083

Rambaut A, Suchard MA, Xie D, Drummond AJ (2014) Tracer v1.6. http://beast.bio.ed.ac.uk/Tracer [Accessed on 27.06.2021]

Rashmi M, Kushveer JS, Sarma VV (2019) A worldwide list of endophytic fungi with notes on ecology and diversity. Mycosphere 10(1): 798–1079. https://doi.org/10.5943/mycosphere/10/1/19

Samuels GJ, Müller E (1979) Life-history studies of Brazilian ascomycetes. 7. *Rhytidhysteron rufulum* and the genus *Eutryblidiella*. Sydowia 31: 277–291.

Schoch CL, Crous PW, Groenewald J, Barres B, Boehm E, de Gruyter J, de Hoog G, Dixon LJ, Fournier J, Grube M, Gueidan C, Harada Y, Hatakeyama S, Hirayama K, Hosoya T, Hyde KD, Jones EBG, Kohlmeyer J, Lucking R, Lumbsch H, Lutzoni F, Marvanova L, Mbatchou J, Miller A, Mugambi G, Muggia L, Nelson M, Nelson P, Owensby C, Phongpaichit S, Pointing S, Pujade-Renaud V, Raja H, Rivas-Plata E, Robbertse B, Ruibal C, Sakayaroj J, Sano T, Selbmann L, Shearer C, Shirouzu T, Slippers B, Suetrong S, Tanaka K, Volkmann-Kohlmeyer B, Wood A, Woudenberg J, Yonezawa H, Zhang Y, Spatafora J (2009) A class wide phylogenetic assessment of Dothideomycetes. Studies in Mycology 64: 1–15. https://doi.org/10.3114/sim.2009.64.01

Schoch CL, Seifert KA, Huhndorf SM, Robert V, Spouge JL, Levesque CA, Chen W, Fungal Barcoding Consortium (2012) Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. Proceedings of the National Academy of Sciences. 109(16): 6241–6246. https://doi.org/10.1073/pnas.1117018109

Soto-Medina E, Lücking R (2017) A new species of *Rhytidhysteron* (Ascomycota: Patellariaceae) from Colombia, with a provisional working key to known species in the world. Revista de la Academia Colombiana de Ciencias Exactas, Físicas y Naturales 41: 59–63. https://doi.org/10.18257/raccefyn.423

Spegazzini C (1881) Fungi argentini additis nonnullis brasiliensibus montevideensibusque. Pugillus IV. Anales de la Sociedad Científica Argentina 12(4): 174–189. [nos 155–193].

Thambugala KM, Hyde KD, Eungwanichayapant PD, Romero AI, Liu Z-Y (2016) Additions to the genus *Rhytidhysteron* in Hysteriaceae. Cryptogamie Mycologie 37: 99–116. https://doi.org/10.7872/crym/v37.iss1.2016.99

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172: 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR Protocols: a guide to methods and applications. Academic Press, San Diego, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L, Haelewaters D, Rajeshkumar KC, Zhao RL, Aptroot A, Leontyev DV, Saxena RK, Tokarev YS, Dai DQ, Letcher PM, Stephenson SL, Ertz D, Lumbsch HT, Kukwa M, Issi IV, Madrid H, Phillips AJL, Selbmann L, Pfliegler WP, Horváth E, Bensch K, Kirk PM, Kolaříková K, Raja HA, Radek R, Papp V, Dima V, Ma J, Malosso E, Takamatsu S, Rambold G, Gannibal PB, Triebel D, Gautam AK, Avasthi S, Suetrong S, Timdal E, Fryar SC, Delgado G, Réblová M, Doilom M, Dolatabadi S, Pawłowska J, Humber RA, Kodsueb R, Sánchez-Castro I, Goto BT, Silva DKA, de Souza FA, Oehl F, da Silva GA, Silva IR, Błaszkowski J, Jobim K, Maia LC, Barbosa FR, Fiuza PO, Divakar PK, Shenoy BD, Castañeda-Ruiz RF, Somrithipol S, Lateef AA, Karunarathna SC, Tibpromma S, Mortimer PE, Wanasinghe DN, Phookamsak R, Xu J, Wang Y, Tian F, Alvarado P, Li DW, Kušan I, Matočec N, Maharachchikumbura SSN, Papizadeh M, Heredia G, Wartchow F, Bakhshi M, Boehm E, Youssef N, Hustad VP, Lawrey JD, Santiago ALCMA, Bezerra JDP, Souza-Motta CM, Firmino AL, Tian Q, Houbraken J, Hongsanan S, Tanaka K, Dissanayake AJ, Monteiro JS, Grossart HP, Suija A, Weerakoon G, Etayo J, Tsurykau A, Vázquez V, Mungai P, Damm U, Li QR, Zhang H, Boonmee S, Lu YZ, Becerra AG, Kendrick B, Brearley FQ, Motiejūnaitė J, Sharma B, Khare R, Gaikwad S, Wijesundara DSA, Tang LZ, He MQ, Flakus A, Rodriguez-Flakus P, Zhurbenko MP, McKenzie EHC, Stadler M, Bhat DJ, Liu JK, Raza M, Jeewon R, Nassonova ES, Prieto M, Jayalal RGU, Erdoğdu M, Yurkov A, Schnittler M, Shchepin ON, Novozhilov YK, Silva-Filho AGS, Liu P, Cavender JC, Kang Y, Mohammad S, Zhang LF, Xu RF, Li YM, Dayarathne MC, Ekanayaka AH, Wen TC, Deng CY, Pereira OL, Navathe S, Hawksworth DL, Fan XL, Dissanayake LS, Kuhnert E, Grossart HP, Thines M (2020) Outline of fungi and fungus-like taxa. Mycosphere 11(1): 1060–1456, https://doi.org/10.5943/mycosphere/11/1/8

Wu G, Feng B, Xu J, Zhu XT, Li YC, Zeng NK, Hosen MI, Yang Z (2014) Molecular phylogenetic analyses redefine seven major clades and reveal 25 new generic lineages in the fungal family Boletaceae. Fungal Diversity 69: 93–115. https://doi.org/10.1007/s13225-014-0283-8

Yacharoen S, Tian Q, Chomnunti P, Boonmee S, Chukeatirote E, Bhat JD, Hyde KD (2015) Patellariaceae revisited. Mycosphere 6: 290–326. https://doi.org/10.5943/mycosphere/6/3/7

Zhang Z, Schwartz S, Wagner L, Miller W (2000) A greedy algorithm for aligning DNA sequences. Journal of Computational Biology 7: 203–214. https://doi.org/10.1089/10665270050081478